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(54) Title: COMPOSITIONS AND METHODS FOR GENETIC MODIFICATION OF PLANTS (57) Abstract Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical recombination sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical recombination sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the recombination sites is effected by a recombinase.		

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COMPOSITIONS AND METHODS FOR GENETIC MODIFICATION OF PLANTS

CROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims the benefit of U.S. Application Serial No. 60/065,627, filed November 18, 1997, and U.S. Application Serial No. 60/065,613, filed November 18, 1997, both of which are herein incorporated by reference.

FIELD OF THE INVENTION

10 The invention relates to the genetic modification of plants. Particularly, the control of gene integration and expression in plants is provided.

BACKGROUND OF THE INVENTION

15 Genetic modification techniques enable one to insert exogenous nucleotide sequences into an organism's genome. A number of methods have been described for the genetic modification of plants. All of these methods are based on introducing a foreign DNA into the plant cell, isolation of those cells containing the foreign DNA integrated into the genome, followed by subsequent regeneration of a whole plant. Unfortunately, such methods produce transformed cells that contain the introduced foreign DNA inserted
20 randomly throughout the genome and often in multiple copies.

The random insertion of introduced DNA into the genome of host cells can be lethal if the foreign DNA happens to insert into, and thus mutate, a critically important native gene. In addition, even if a random insertion event does not impair the functioning of a host cell gene, the expression of an inserted foreign gene may be influenced by
25 "position effects" caused by the surrounding genomic DNA. In some cases, the gene is inserted into sites where the position effects are strong enough to prevent the synthesis of an effective amount of product from the introduced gene. In other instances, overproduction of the gene product has deleterious effects on the cell.

Transgene expression is typically governed by the sequences, including promoters and enhancers, which are physically linked to the transgene. Currently, it is not possible to precisely modify the structure of transgenes once they have been introduced into plant cells. In many applications of transgene technology, it would be desirable to introduce the
5 transgene in one form, and then be able to modify the transgene in a defined manner. By this means, transgenes could be activated or inactivated where the sequences that control transgene expression can be altered by either removing sequences present in the original transgene or by inserting additional sequences into the transgene.

For higher eukaryotes, homologous recombination is an essential event participating
10 in processes like DNA repair and chromatid exchange during mitosis and meiosis. Recombination depends on two highly homologous extended sequences and several auxiliary proteins. Strand separation can occur at any point between the regions of homology, although particular sequences may influence efficiency. These processes can be exploited for a targeted integration of transgenes into the genome of certain cell types.

15 Even with the advances in genetic modification of higher plants, the major problems associated with the conventional gene transformation techniques have remained essentially unresolved as to the problems discussed above relating to variable expression levels due to chromosomal position effects and copy number variation of transferred genes.

For these reasons, efficient methods are needed for targeting and control of insertion of
20 nucleotide sequences to be integrated into a plant genome.

SUMMARY OF THE INVENTION

Compositions and methods for the targeted integration of nucleotide sequences into a transformed plant are provided. The compositions comprise transfer cassettes which are
25 flanked by non-identical recombination sites.

The methods find use in targeting the integration of nucleotide sequences of interest to a specific chromosomal site, finding optimal integration sites in a plant genome, comparing promoter activity in transformed plants, engineering chromosomal rearrangements, and other genetic manipulation of plants.

30 Novel minimal recombination sites (FRT) are provided for use in the methods of the invention. Also provided are targeting cassettes and transgenic plants and plant cells containing corresponding non-identical recombination sites.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 provides one scheme for gene stacking via site-specific integration using the FLP system.

Figure 2 provides a construct of the representative plasmid PHP10616.

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DETAILED DESCRIPTION OF THE INVENTION

Compositions and methods for the directional, targeted integration of exogenous nucleotides into a transformed plant are provided. The methods use novel recombination sites in a gene targeting system which facilitates directional targeting of desired genes and
10 nucleotide sequences into corresponding recombination sites previously introduced into the target plant genome.

In the methods of the invention, a nucleotide sequence flanked by two non-identical recombination sites is introduced into the target organism's genome establishing a target site for insertion of nucleotide sequences of interest. Once a stable plant or cultured tissue
15 is established a second construct, or nucleotide sequence of interest, flanked by corresponding recombination sites as those flanking the target site, is introduced into the stably transformed plant or tissues in the presence of a recombinase protein. This process results in exchange of the nucleotide sequences between the non-identical recombination sites of the target site and the transfer cassette.

20 It is recognized that the transformed plant may comprise multiple target sites; *i.e.*, sets of non-identical recombination sites. In this manner, multiple manipulations of the target site in the transformed plant are available. By target site in the transformed plant is intended a DNA sequence that has been inserted into the transformed plant's genome and comprises non-identical recombination sites.

25 Examples of recombination sites for use in the invention are known in the art and include FRT sites (See, for example, Schlake and Bode (1994) *Biochemistry* 33:12746-12751; Huang *et al.* (1991) *Nucleic Acids Research* 19:443-448; Paul D. Sadowski (1995) *In Progress in Nucleic Acid Research and Molecular Biology* vol. 51, pp. 53-91; Michael M. Cox (1989) *In Mobile DNA*, Berg and Howe (eds) American Society of Microbiology, Washington D.C., pp. 116-670; Dixon *et al.* (1995) 18:449-458; Umlauf and Cox (1988)
30 *The EMBO Journal* 7:1845-1852; Buchholz *et al.* (1996) *Nucleic Acids Research* 24:3118-3119; Kilby *et al.* (1993) *Trends Genet.* 9:413-421; Rossant and Geagy (1995) *Nat. Med.* 1: 592-594; Albert *et al.* (1995) *The Plant J.* 7:649-659; Bayley *et al.* (1992) *Plant Mol. Biol.* 18:353-361; Odell *et al.* (1990) *Mol. Gen. Genet.* 223:369-378; and Dale and Ow

(1991) *Proc. Natl. Acad. Sci. USA* 88:10558-105620; all of which are herein incorporated by reference.); *Lox* (Albert *et al.* (1995) *Plant J.* 7:649-659; Qui *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:1706-1710; Stuurman *et al.* (1996) *Plant Mol. Biol.* 32:901-913; Odell *et al.* (1990) *Mol. Gen. Gevet.* 223:369-378; Dale *et al.* (1990) *Gene* 91:79-85; and Bayley *et al.* (1992) *Plant Mol. Biol.* 18:353-361.)

The two-micron plasmid found in most naturally occurring strains of *Saccharomyces cerevisiae*, encodes a site-specific recombinase that promotes an inversion of the DNA between two inverted repeats. This inversion plays a central role in plasmid copy-number amplification. The protein, designated FLP protein, catalyzes site-specific recombination events. The minimal recombination site (FRT, SEQ ID NO 1) has been defined and contains two inverted 13-base pair (bp) repeats surrounding an asymmetric 8-bp spacer. The FLP protein cleaves the site at the junctions of the repeats and the spacer and is covalently linked to the DNA via a 3' phosphate.

Site specific recombinases like FLP cleave and religate DNA at specific target sequences, resulting in a precisely defined recombination between two identical sites. To function, the system needs the recombination sites and the recombinase. No auxiliary factors are needed. Thus, the entire system can be inserted into and function in plant cells.

The yeast FLP\FRT site specific recombination system has been shown to function in plants. To date, the system has been utilized for excision of unwanted DNA. See, Lyznik *et al.* (1993) *Nucleic Acid Res.* 21:969-975. In contrast, the present invention utilizes non-identical FRTs for the exchange, targeting, arrangement, insertion and control of expression of nucleotide sequences in the plant genome.

To practice the methods of the invention, a transformed organism of interest, particularly a plant, containing a target site integrated into its genome is needed. The target site is characterized by being flanked by non-identical recombination sites. A targeting cassette is additionally required containing a nucleotide sequence flanked by corresponding non-identical recombination sites as those sites contained in the target site of the transformed organism. A recombinase which recognizes the non-identical recombination sites and catalyzes site-specific recombination is required.

It is recognized that the recombinase can be provided by any means known in the art. That is, it can be provided in the organism or plant cell by transforming the organism with an expression cassette capable of expressing the recombinase in the organism, by transient expression; or by providing messenger RNA (mRNA) for the recombinase or the recombinase protein.

By "non-identical recombination sites" is intended that the flanking recombination sites are not identical in sequence and will not recombine or recombination between the sites will be minimal. That is, one flanking recombination site may be a FRT site where the second recombination site may be a mutated FRT site. The non-identical recombination sites used in the methods of the invention prevent or greatly suppress recombination between the two flanking recombination sites and excision of the nucleotide sequence contained therein. Accordingly, it is recognized that any suitable non-identical recombination sites may be utilized in the invention, including FRT and mutant FRT sites, FRT and lox sites, lox and mutant lox sites, as well as other recombination sites known in the art.

By suitable non-identical recombination site implies that in the presence of active recombinase, excision of sequences between two non-identical recombination sites occurs, if at all, with an efficiency considerably lower than the recombinationally-mediated exchange targeting arrangement of nucleotide sequences into the plant genome. Thus, suitable non-identical sites for use in the invention include those sites where the efficiency of recombination between the sites is low; for example, where the efficiency is less than about 30 to about 50%, preferably less than about 10 to about 30%, more preferably less than about 5 to about 10%.

As noted above, the recombination sites in the targeting cassette correspond to those in the target site of the transformed plant. That is, if the target site of the transformed plant contains flanking non-identical recombination sites of FRT and a mutant FRT, the targeting cassette will contain the same FRT and mutant FRT non-identical recombination sites.

It is furthermore recognized that the recombinase, which is used in the invention, will depend upon the recombination sites in the target site of the transformed plant and the targeting cassette. That is, if FRT sites are utilized, the FLP recombinase will be needed.

In the same manner, where lox sites are utilized, the Cre recombinase is required. If the non-identical recombination sites comprise both a FRT and a lox site, both the FLP and Cre recombinase will be required in the plant cell.

The FLP recombinase is a protein which catalyzes a site-specific reaction that is involved in amplifying the copy number of the two micron plasmid of *S. cerevisiae* during DNA replication. FLP protein has been cloned and expressed. See, for example, Cox (1993) Proc. Natl. Acad. Sci. U.S.A. 80:4223-4227. The FLP recombinase for use in the invention may be that derived from the genus *Saccharomyces*. It may be preferable to

synthesize the recombinase using plant preferred codons for optimum expression in a plant of interest. See, for example, U.S. Application Serial No. 08/972,258 filed November 18, 1997, entitled "Novel Nucleic Acid Sequence Encoding FLP Recombinase", herein incorporated by reference.

5 The bacteriophage recombinase Cre catalyzes site-specific recombination between two lox sites. The Cre recombinase is known in the art. See, for example, Guo *et al.* (1997) *Nature* 389:40-46; Abremski *et al.* (1984) *J. Biol. Chem.* 259:1509-1514; Chen *et al.* (1996) *Somat. Cell Mol. Genet.* 22:477-488; and Shaikh *et al.* (1977) *J. Biol. Chem.* 272:5695-5702. All of which are herein incorporated by reference. Such Cre sequence
10 may also be synthesized using plant preferred codons.

 Where appropriate, the nucleotide sequences to be inserted in the plant genome may be optimized for increased expression in the transformed plant. Where mammalian, yeast, or bacterial genes are used in the invention, they can be synthesized using plant preferred codons for improved expression. It is recognized that for expression in monocots, dicot
15 genes can also be synthesized using monocot preferred codons. Methods are available in the art for synthesizing plant preferred genes. See, for example, U.S. Patent Nos. 5,380,831, 5,436, 391, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

 The plant preferred codons may be determined from the codons utilized more
20 frequently in the proteins expressed in the plant of interest. It is recognized that monocot or dicot preferred sequences may be constructed as well as plant preferred sequences for particular plant species. See, for example, EPA 0359472; EPA 0385962; WO 91/16432; Perlak *et al.* (1991) *Proc. Natl. Acad. Sci. USA*, 88:3324-3328; and Murray *et al.* (1989) *Nucleic Acids Research*, 17: 477-498. U.S. Patent No. 5,380,831; U.S. Patent No.
25 5,436,391; and the like, herein incorporated by reference. It is further recognized that all or any part of the gene sequence may be optimized or synthetic. That is, fully optimized or partially optimized sequences may also be used.

 Additional sequence modifications are known to enhance gene expression in a cellular host and can be used in the invention. These include elimination of sequences
30 encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences, which may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

The present invention also encompasses novel FLP recombination target sites (FRT). The FRT (SEQ ID NO 1) has been identified as a minimal sequence comprising two 13 base pair repeats, separated by an 8 base spacer, as follows:

5'-GAAGTTCCTATTC[TCTAGAAA]GTATAGGAACTTC3'

5 wherein the nucleotides within the brackets indicate the spacer region. The nucleotides in the spacer region can be replaced with a combination of nucleotides, so long as the two 13-base repeats are separated by eight nucleotides. It appears that the actual nucleotide sequence of the spacer is not critical, however for the practice of the invention, some substitutions of nucleotides in the space region may work better than others.

10 The eight base pair spacer is involved in DNA-DNA pairing during strand exchange. The asymmetry of the region determines the direction of site alignment in the recombination event, which will subsequently lead to either inversion or excision. As indicated above, most of the spacer can be mutated without a loss of function. See, for example, Schlake and Bode (1994) Biochemistry 33:12746-12751, herein incorporated by
15 reference.

Novel FRT mutant sites are provided for use in the practice of the methods of the present invention. Such mutant sites may be constructed by PCR-based mutagenesis. While mutant FRT sites (SEQ ID Nos 2, 3, 4 and 5) are provided herein, it is recognized that other mutant FRT sites may be used in the practice of the invention. The present
20 invention is not the use of a particular FRT or recombination site, but rather that non-identical recombination sites or FRT sites can be utilized for targeted insertion and expression of nucleotide sequences in a plant genome. Thus, other mutant FRT sites can be constructed and utilized based upon the present disclosure.

As discussed above, bringing genomic DNA containing a target site with non-
25 identical recombination sites together with a vector containing a transfer cassette with corresponding non-identical recombination sites, in the presence of the recombinase, results in recombination. The nucleotide sequence of the transfer cassette located between the flanking recombination sites is exchanged with the nucleotide sequence of the target site located between the flanking recombination sites. In this manner, nucleotide sequences of
30 interest may be precisely incorporated into the genome of the host.

It is recognized that many variations of the invention can be practiced. For example, target sites can be constructed having multiple non-identical recombination sites. Thus, multiple genes or nucleotide sequences can be stacked or ordered at precise locations in the plant genome. Likewise, once a target site has been established within the

genome, additional recombination sites may be introduced by incorporating such sites within the nucleotide sequence of the transfer cassette and the transfer of the sites to the target sequence. Thus, once a target site has been established, it is possible to subsequently add sites, or alter sites through recombination.

5 Another variation includes providing a promoter or transcription initiation region operably linked with the target site in an organism. Preferably, the promoter will be 5' to the first recombination site. By transforming the organism with a transfer cassette comprising a coding region, expression of the coding region will occur upon integration of the transfer cassette into the target site. This embodiment provides for a method to
10 select transformed cells, particularly plant cells, by providing a selectable marker sequence as the coding sequence.

Other advantages of the present system include the ability to reduce the complexity of integration of trans-genes or transferred DNA in an organism by utilizing transfer cassettes as discussed above and selecting organisms with simple integration patterns. In
15 the same manner, preferred sites within the genome can be identified by comparing several transformation events. A preferred site within the genome includes one that does not disrupt expression of essential sequences and provides for adequate expression of the transgene sequence.

The methods of the invention also provide for means to combine multiple cassettes
20 at one location within the genome. See, for example, Figure 1. Recombination sites may be added or deleted at target sites within the genome.

Any means known in the art for bringing the three components of the system together may be used in the invention. For example, a plant can be stably transformed to harbor the target site in its genome. The recombinase may be transiently expressed or
25 provided. Alternatively, a nucleotide sequence capable of expressing the recombinase may be stably integrated into the genome of the plant. In the presence of the corresponding target site and the recombinase, the transfer cassette, flanked by corresponding non-identical recombination sites, is inserted into the transformed plant's genome.

Alternatively, the components of the system may be brought together by sexually
30 crossing transformed plants. In this embodiment, a transformed plant, parent one, containing a target site integrated in its genome can be sexually crossed with a second plant, parent two, that has been genetically transformed with a transfer cassette containing flanking non-identical recombination sites, which correspond to those in plant one. Either plant one or plant two contains within its genome a nucleotide sequence expressing

recombinase. The recombinase may be under the control of a constitutive or inducible promoter.

Inducible promoters include heat-inducible promoters, estradiol-responsive promoters, chemical inducible promoters, and the like. Pathogen inducible promoters
5 include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; e.g., PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, etc. See, for example, Redolfi *et al.* (1983) *Neth. J. Plant Pathol.* 89:245-254; Uknes *et al.* (1992) *The Plant Cell* 4:645-656; and Van Loon (1985) *Plant Mol. Virol.* 4:111-116. In this manner, expression of recombinase and subsequent activity at the
10 recombination sites can be controlled.

Constitutive promoters for use in expression of genes in plants are known in the art. Such promoters include, but are not limited to 35S promoter of cauliflower mosaic virus (Depicker *et al.* (1982) *Mol. Appl. Genet.* 1:561-573; Odell *et al.* (1985) *Nature* 313:810-812), ubiquitin promoter (Christensen *et al.* (1992) *Plant Mol. Biol.* 18:675-689),
15 promoters from genes such as ribulose biphosphate carboxylase (De Almeida *et al.* (1989) *Mol. Gen. Genet.* 218:78-98), actin (McElroy *et al.* (1990) *Plant J.* 2:163-171), histone, DnaJ (Baszczynski *et al.* (1997) *Maydica* 42:189-201), and the like.

The compositions and methods of the invention find use in targeting the integration of transferred nucleotide sequences to a specific chromosomal site. The nucleotide
20 sequence may encode any nucleotide sequence of interest. Particular genes of interest include those which provide a readily analyzable functional feature to the host cell and/or organism, such as marker genes, as well as other genes that alter the phenotype of the recipient cells, and the like. Thus, genes effecting plant growth, height, susceptibility to disease, insects, nutritional value, and the like may be utilized in the invention. The
25 nucleotide sequence also may encode an 'antisense' sequence to turn off or modify gene expression.

It is recognized that the nucleotide sequences will be utilized in a functional expression unit or cassette. By functional expression unit or cassette is intended, the nucleotide sequence of interest with a functional promoter, and in most instances a
30 termination region. There are various ways to achieve the functional expression unit within the practice of the invention. In one embodiment of the invention, the nucleic acid of interest is transferred or inserted into the genome as a functional expression unit. Alternatively, the nucleotide sequence may be inserted into a site within the genome which

is 3' to a promoter region. In this latter instance, the insertion of the coding sequence 3' to the promoter region is such that a functional expression unit is achieved upon integration. For convenience, for expression in plants, the nucleic acid encoding target sites and the transfer cassettes, including the nucleotide sequences of interest, can be contained within expression cassettes. The expression cassette will comprise a transcriptional initiation region, or promoter, operably linked to the nucleic acid encoding the peptide of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene or genes of interest to be under the transcriptional regulation of the regulatory regions.

The transcriptional initiation region, the promoter, may be native or homologous or foreign or heterologous to the host, or could be the natural sequence or a synthetic sequence. By foreign is intended that the transcriptional initiation region is not found in the wild-type host into which the transcriptional initiation region is introduced. Either a native or heterologous promoter may be used with respect to the coding sequence of interest.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the potato proteinase inhibitor (PinII) gene or from Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau *et al.*, (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* 1989) *Nucleic Acids Res.* 17:7891-7903; Joshi *et al.* (1987) *Nucleic Acid Res.* 15:9627-9639.

The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein, O., Fuerst, T.R., and Moss, B. (1989) *PNAS USA*, 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.* (1986); MDMV leader (Maize Dwarf Mosaic Virus); *Virology*, 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP), (Macejak, D.G., and P. Sarnow (1991) *Nature*, 353:90-94; untranslated leader from

the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling, S.A., and Gehrke, L., (1987) *Nature*, 325:622-625; tobacco mosaic virus leader (TMV), (Gallie *et al.* (1989) *Molecular Biology of RNA*, pages 237-256, Gallie *et al.* (1987) *Nucl. Acids Res.* 15:3257-3273; and maize chlorotic mottle virus leader (MCMV) (Lommel, S.A. *et al.* 5 (1991) *Virology*, 81:382-385). See also, Della-Cioppa *et al.* (1987) *Plant Physiology*, 84:965-968. Other methods known to enhance translation can also be utilized, for example, introns, and the like.

The expression cassettes may contain one or more than one gene or nucleic acid sequence to be transferred and expressed in the transformed plant. Thus, each nucleic acid 10 sequence will be operably linked to 5' and 3' regulatory sequences. Alternatively, multiple expression cassettes may be provided.

Generally, the expression cassette will comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or tissues.

15 See generally, G. T. Yarranton (1992) *Curr. Opin. Biotech.*, 3:506-511; Christopherson *et al.* (1992) *Proc. Natl. Acad. Sci. USA*, 89:6314-6318; Yao *et al.* (1992) *Cell*, 71:63-72; W. S. Reznikoff (1992) *Mol. Microbiol.*, 6:2419-2422; Barkley *et al.* (1980) *The Operon*, pp. 177-220; Hu *et al.* (1987) *Cell*, 48:555-566; Brown *et al.* (1987) *Cell*, 49:603-612; Figge *et al.* (1988) *Cell*, 52:713-722; Deuschle *et al.* (1989) *Proc. Natl.* 20 *Acad. Sci. USA*, 86:5400-5404; Fuerst *et al.* (1989) *Proc. Natl. Acad. Sci. USA*, 86:2549-2553; Deuschle *et al.* (1990) *Science*, 248:480-483; M. Gossen (1993) PhD Thesis, University of Heidelberg; Reines *et al.* (1993) *Proc. Natl. Acad. Sci. USA*, 90:1917-1921; Labow *et al.* (1990) *Mol. Cell Bio.*, 10:3343-3356; Zambretti *et al.* (1992) *Proc. Natl. Acad. Sci. USA*, 89:3952-3956; Baim *et al.* (1991) *Proc. Natl. Acad. Sci. USA*, 88:5072- 25 5076; Wyborski *et al.* (1991) *Nucl. Acids Res.*, 19:4647-4653; A. Hillenand-Wissman (1989) *Topics in Mol. and Struc. Biol.*, 10:143-162; Degenkolb *et al.* (1991) *Antimicrob. Agents Chemother.*, 35:1591-1595; Kleinschmidt *et al.* (1988) *Biochemistry*, 27:1094-1104; Gatz *et al.* (1992) *Plant J.*, 2:397-404; A. L. Bonin (1993) PhD Thesis, University of Heidelberg; Gossen *et al.* (1992) *Proc. Natl. Acad. Sci. USA*, 89:5547-5551; Oliva *et al.* 30 (1992) *Antimicrob. Agents Chemother.*, 36:913-919; Hlavka *et al.* (1985) *Handbook of Exp. Pharmacology*, 78; Gill *et al.* (1988) *Nature* 334:721-724. Such disclosures are herein incorporated by reference.

The methods of the invention can also be utilized to find optimal integration sites within a plant genome. In this manner, a plant is transformed with an expression cassette

comprising a selectable marker gene. The expression cassette is a target site as the marker gene is flanked by non-identical recombination sites. Transformed protoplast, tissues, or whole plants can be tested to determine the levels of activity of the inserted gene. By comparison of cellular activities of the gene in different insertion sites, preferred
5 integration sites may be found wherein the gene is expressed at high or acceptable levels. These plants can then be utilized with subsequent retargeting techniques to replace the marker gene with other genes or nucleotide sequences of interest. In the same manner, multiple genes may be inserted at the optimal site for expression. See, for example, Figure 2 which sets forth one scheme for gene stacking utilizing site-specific integration using the
10 FRT/FLP system.

A variety of genetic manipulations are available using the compositions of the present invention including, for example, comparing promoter activity in a transformed plant. Prior to the present invention, promoter activity could not accurately be assessed and compared because the chimeric genes were inserted at different locations within the plant
15 genome. Such chromosomal locations affected activity. By utilizing the methods of the present invention, a direct comparison of promoter activity in a defined chromosomal context is possible. Thus, using the methods, enhanced activity of genes can be achieved by selecting optimal chromosomal sites as well as optimal promoters for expression in the plant cell.

The present invention may be used for transformation of any plant species, including but not limited to corn (*Zea mays*), canola (*Brassica napus*, *Brassica rapa* ssp.), alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), sunflower (*Helianthus annuus*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum
25 tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea
30 europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), oats, barley, vegetables, ornamentals, and conifers.

Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca*

sativa), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.) and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers which may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Preferably, plants of the present invention are crop plants (for example, corn, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, wheat, tobacco, etc.), more preferably corn and soybean plants, yet more preferably corn plants.

It is recognized that the methods of the invention may be applied in any plant system. Methods for transformation of plants are known in the art. In this manner, genetically modified plants, plant cells, plant tissue, seed, and the like can be obtained. Transformation protocols may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of transforming plant cells include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA*, 83:5602-5606, *Agrobacterium* mediated transformation (Hinchee *et al.* (1988) *Biotechnology*, 6:915-921), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.*, 3:2717-2722), and ballistic particle acceleration (see, for example, Sanford *et al.*, U.S. Patent 4,945,050; WO91/10725 and McCabe *et al.* (1988) *Biotechnology*, 6:923-926). Also see, Weissinger *et al.* (1988) *Annual Rev. Genet.*, 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology*, 5:27-37 (onion); Christou *et al.* (1988) *Plant Physiol.* 87:671-674(soybean); McCabe *et al.* (1988) *Bio/Technology*, 6:923-926 (soybean); Datta *et al.* (1990) *Biotechnology*, 8:736-740(rice); Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA*, 85:4305-4309(maize); Klein *et al.* (1988) *Biotechnology*, 6:559-563 (maize); WO91/10725 (maize); Klein *et al.* (1988) *Plant Physiol.*, 91:440-444(maize); Fromm *et*

al. (1990) *Biotechnology*, 8:833-839; and Gordon-Kamm *et al.* (1990) *Plant Cell*, 2:603-618 (maize); Hooxdaas-Van Slooteren & Hooxkaas (1984) *Nature (London)*, 311:763-764; Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA*, 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) In *The Experimental Manipulation of Ovule Tissues*, ed. G.P. Chapman *et al.*, pp. 197-209. Longman, NY (pollen); Kaeppler *et al.* (1990) *Plant Cell Reports*, 9:415-418; and Kaeppler *et al.* (1992) *Theor. Appl. Genet.*, 84:560-566 (whisker-mediated transformation); D'Halluin *et al.* (1992) *Plant Cell*, 4:1495-1505 (electroporation); Li *et al.* (1993) *Plant Cell Reports*, 12:250-255 and Christou and Ford (1995) *Annals of Botany*, 75:407-413 (rice); Osjoda *et al.* (1996) *Nature Biotechnology*, 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

The cells which have been transformed may be grown into plants in accordance with conventional approaches. See, for example, McCormick *et al.* (1986) *Plant Cell Reports*, 5:81-84. These regenerated plants may then be pollinated with either the same transformed strain or different strains, and the resulting hybrid having the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that the subject phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure the desired phenotype or other property has been achieved.

It is recognized that any means of transformation may be utilized for the present invention. However, for inserting the target site within the transformed plant, *Agrobacterium*-mediated transformation may be preferred. *Agrobacterium*-mediated transformation generally tends to insert a lower copy number of transferred DNA than does particle bombardment or other transformation means.

The following examples are offered by way of illustration and not by way of limitation.

Experimental

The general present invention provides a procedure for using existing and novel FRT sites in a new gene targeting system which facilitates directional retargeting of desired genes into FRT sites previously introduced in the target organism's genome. The novel FRT sites differ from previously described FRT sites in the sequence of the 8 bp spacer regions of the FRT sites. Previous publications also have shown that in the presence of FLP protein, recombination of sequences between two FRT sites occurs efficiently only with two identical FRT sites. See for example Umlauf and Cox (1988) *Embo J.* 7:1845-1852; Schlake and Bode (1994) *Biochem.* 33:12746-12751. To use the invention, a gene or DNA sequence is flanked by two non-identical FRT sites and introduced into a target organism's genome. The enclosed gene can be a selectable marker, thereby allowing selection for successfully introduced sequences. Molecular characterization confirms integration of desired sequences including complete FRT sites. Listed below are generic examples of vector constructions useful in practicing the invention:

15

- A. FRT_a-P1-G1-T1-FRT_b
- B. FRT_a-P1-G1-T1-FRT_a
- C. FRT_b-P1-G1-T1-FRT_b
- D. P1-FRT_a-G1-T1-FRT_b
- 20 E. P1-FRT_a-G1-T1-FRT_a
- F. P1-FRT_b-G1-T1-FRT_b
- G. P1-ATG::FRT_a::G1(noATG)-T1-P2-G2-T2-FRT_b
- H. P1-ATG::FRT_a::G1(noATG)-T1-P2-G2-T2-FRT_b-P3-G3-T3
- I. P1-ATG::FRT_a::G1(noATG)-T1-FRT_a::G2(noATG)-T2-FRT_b
- 25 J. P1-ATG::FRT_a::G1(noATG)-T1-FRT_a::G2(noATG)-T2-FRT_b-P3-G3-T3
- K. P1-FRT_a-G1-T1-P2-G2-T2-FRT_b
- L. P1-FRT_a-G1-T1-P2-G2-T2-FRT_b-P3-G3-T3
- M. P1-FRT_a-G1-T1-FRT_a-G2-T2-FRT_b
- N. P1-FRT_a-G1-T1-FRT_a-G2-T2-FRT_b-P3-G3-T3

30

Variations thereof may be constructed with other promoters, genes, terminators or FRT sites.

FRTa and FRTb are two examples of non-identical FRT sites. P1, P2 and P3 are different promoters, G1, G2, and G3 are different genes, T1, T2 and T3 are different terminators. ATG is the start of translation codon for the subsequent gene. The designation noATG indicates that particular gene is devoid of the ATG translation start codon. The symbol :: implies a fusion between adjacent elements, and where used between ATG, FRT and a gene, implies that the sequences are put together to generate an in frame translation fusion that results in a properly expressed and functional gene product.

A to F are preferred configurations for testing new FRT sites for ability to recombine sequences between them; the desired situation being that when two of the same site are used, recombination is efficient and that when two different sites are used, no recombination between them takes place in the presence of FLP protein. G to J are preferred configurations for general use in developing lines for retargeting. It is understood that any number of genes or other combinations of sequences can be assembled for use as part of this invention. K to N are possible configurations that could be used also.

Once a stable plant or cultured tissue is established with one of the constructs above, a second construct flanked by the same FRT sites used to flank the sequences in the first construct above is introduced into the stably transformed tissues in conjunction with the expression of FLP protein. The new vector constructs can be, but are not limited to the following:

- O. FRTa::G1(noATG)-T1-FRTb
- P. FRTa::G1(noATG)-T1-P2-G2-T2-FRTb
- Q. FRTa-G1-T1-FRTb
- 25 R. FRTa-G1-T1-P2-G2-T2-FRTb

The FLP protein can be supplied by a) co-transforming with a plasmid carrying a gene encoding FLP; b) co-introducing FLP mRNA or protein directly; c) using a line for the initial transformation that expresses FLP either constitutively or following induction; or
30 d) growing out the plants carrying the initial targeted vectors, crossing to plants that express active FLP protein and selecting events in the progeny.

As a working example, sequence O above is introduced into a line containing a copy of sequence G stably integrated in the genome, in the presence of functional FLP protein. Recombination takes place between identical FRT sites such that the sequence

between FRT sites in O replaces the sequence between the corresponding FRT sites of sequence G, thereby yielding a directionally targeted reintegrated new sequence. The new gene in O is now driven off of the P1 promoter in G. The purpose for designing some of the constructs without an ATG start codon on the gene is so that if random integration occurs, there is an extremely low probability of expression of the introduced gene, since in order for this to happen, the fragment would need to integrate behind an endogenous promoter region and in the correct reading frame. This would occur extremely rarely and our data to date have yielded no examples of this happening using a sequence such as O where the contained gene is the easily scorable GUS gene. One requirement for each gene to be constructed in this way (i.e., no ATG on the gene but with the ATG upstream of the FRT site) is the demonstration that the gene can tolerate a fusion of the FRT sequence between the ATG codon and the second codon of the protein. To date this has worked for quite a number but not all genes; in the latter cases the other form of the construct retaining the ATG (for example Q.) could be used. All of the sequences listed above are expected to work in this scheme, some at different frequencies or efficiencies than others.

One problem this strategy addresses is limitations with current transformation approaches, particularly in plants, where delivery of DNA into cells or nuclei and subsequent integration in the genome occurs more or less randomly and unpredictably. This is particularly true with particle bombardment methods; arguments have been made that *Agrobacterium*-based methods tend to deliver T-DNA border-flanked sequences to more actively transcribed regions of the genome, but beyond that the process is still largely random. Therefore, for commercial product development, large numbers (estimates of > 200) of events need to be generated in order to identify one event: a) that expresses at the desired level; b) where the gene product is functional and efficacious; c) which has a simple integration complexity to facilitate breeding; d) which does not contain extraneous sequences posing possible regulatory concerns; e) which maintains stability in expression over generations; f) most importantly, which does not have a negative impact on agronomic performance characteristics when carried through a breeding program involving introgression of the trait into different genetic backgrounds. Resource utilization is very large and so schemes that can markedly reduce the resource demand would be very beneficial to production of larger numbers of desired final products.

Example 1. Creation of novel non-identical FRT sites

DNA fragments containing novel FRT sequences were constructed either by synthesizing, annealing and ligating complementary oligonucleotides or by creating primers for PCR amplification (Mullis and Faloona, 1987) of a DNA product containing the new FRT sequence near the 5' end of the PCR product. The newly constructed FRT product includes flanking restriction sites useful for cloning into plant expression units. In general, the 5' end is flanked by an NheI site and a terminal NcoI site. The NcoI site includes the bases ATG, which are advantageously used in newly developed vector constructs as the recognition sequence to initiate an open reading frame. In sequence-based constructs designated noATG/FRT, the NheI site is used for cloning thereby eliminating the upstream ATG in the process. At the 3' end of the FRT sequence, a restriction site is included enabling unique identification of the individual spacer sequences. As specific examples, the wild type FRT site (designated FRT1 here) is cloned with a flanking BglII site, the FRT5 site (spacer TTCAAAAG) has a ScaI site, the FRT6 site (spacer TTCAAAAA) has an AatII site, and the FRT7 site (spacer TTCAATAA) has a SpeI site. The outermost flanking restriction site is an XhoI site and is used to clone a gene of interest into the open reading frame.

The structures and sequences of the FRT sites as designed and/or used in the present invention example are depicted below with positions of restriction sites, repeats and spacer regions indicated.

FRT1 (SEQ ID NO 2)

NcoI	NheI	Repeat 1	Repeat 2	Spacer	Inverted Repeat	BglII	XhoI
5'		CCATGGCTAGC	GAAGTTCCTATTCC	GAAGTTCCTATTTC	TCTAGAAA	GTATAGGAACTTC	AGATCTCGAG

FRT5 (SEQ ID NO 3)

NcoI	NheI	Repeat 1	Repeat 2	Spacer	Inverted Repeat	ScaI	XhoI
5'		CCATGGCTAGC	GAAGTTCCTATTCC	GAAGTTCCTATTTC	TTCAAAAG	GTATAGGAACTTC	AGTACTCGAG

FRT6 (SEQ ID NO 4)

NcoI	NheI	Repeat 1	Repeat 2	Spacer	Inverted Repeat	AatII	XhoI
5'		CCATGGCTAGC	GAAGTTCCTATTCC	GAAGTTCCTATTTC	TTCAAAAA	GTATAGGAACTTC	AGACGTCCTCGAG

FRT7 (SEQ ID NO 5)

NcoI	NheI	Repeat 1	Repeat 2	Spacer	Inverted Repeat	SpeI	XhoI
5'		CCATGGCTAGC	GAAGTTCCTATTCC	GAAGTTCCTATTCTTCAATAA	GTATAGGAACTTC	CACTAGTTCTCGAG	

Example 2. Creation of plant transformation vectors containing novel non-identical FRT sites.

Based on the design of FRT sites as described above, PCR or standard mutagenesis protocols were used to create an XhoI site overlapping the start of a gene sequence to be used for cloning downstream of the FRT site, thereby converting the ATG start codon to GTG. Ligation of an FRT to the mutated gene sequence at XhoI creates a new open reading frame initiating 5' to the FRT. A second FRT sequence can be cloned downstream of the terminator using a variety of methods including PCR or ligation. The FRT/gene/terminator/FRT unit can then be used to make target or substrate constructs.

Targets are created by inserting a promoter at the NcoI site upstream of the first FRT. This maintains a complete open reading frame of the FRT/gene fusion. These target constructs are for use in transformation experiments to create desirable 'target lines'. Substrate vectors are constructed by cloning with the NheI site to truncate the start codon of the FRT /gene unit, thereby eliminating the proper open reading frame. These substrate vectors are used in experiments designed to retarget a new gene flanked by FRT sites into the corresponding FRT sites previously introduced in the target lines. In either case, to create multiple gene cassettes, additional promoter/gene/terminator units are inserted between the terminator and the second FRT in either target or substrate molecules.

Example 3. Demonstration of functionality of novel FRT sites and requirement for two identical sites for efficient recombination of DNA sequences positioned between two FRT sites.

Plasmids containing two identical or two different FRT sequences were assayed for efficiency of recombination of sequences between the FRT sites by transformation into 294-FLP, a version of the *E. coli* strain MM294 with FLP recombinase integrated into the lacZ locus (Buchholz et al. 1996). Strains were grown overnight at 37°C with shaking, allowing for constitutive expression of FLP recombinase in the cultures. The plasmid DNA was isolated using standard procedures and digested with restriction enzymes that create novel restriction fragments following FLP mediated recombination. The extent of recombination between FRT sites was estimated by examining banding patterns on an agarose gel. Table 1 summarizes data from the gel analysis.

Table 1

5

Target Site Combination	Extent of Recombination
FRT1 and FRT1	Complete
FRT5 and FRT5	Extensive, but partially incomplete
FRT6 and FRT6	Complete
FRT7 and FRT7	Complete
FRT1 and FRT5	No recombination
FRT1 and FRT6	No recombination
FRT1 and FRT7	No recombination
FRT5 and FRT6	No recombination
FRT5 and FRT7	No recombination
FRT6 and FRT7	Very small amount of recombination

The results from these studies indicate that excision of sequences between identical FRT sites occurs with high efficiency in general (FRT5, SEQ ID NO 3, appeared to be less efficient overall than FRT1, SEQ ID NO 2, or the novel FRT6, SEQ ID NO 4, and FRT 7, SEQ ID NO 5, sites). As importantly, recombination with two different FRT sites was absent, or at least undetectable under the conditions of this assay for all combinations but FRT6, SEQ ID NO 4, and FRT7, SEQ ID NO 5, where a small degree of recombination was noted. These data provided strong support for the potential utility of non-identical FRT sites in developing a directional gene integration system. A point to note is that because recombination of sequences between two identical FRT sites can occur with different efficiencies depending on the specific FRT site used (e.g., FRT5, SEQ ID NO 3, in the present experiment), the design of constructs for directional targeted integration may require judicious selection of pairs of FRT sites to optimize for the desired recombination efficiency or to avoid any unwanted recombination.

Example 4. Introduction of DNA sequences which include novel non-identical FRT sites into plant cells, generation and recovery of stable transgenic events ('target lines'), preservation of 'target lines' and regeneration of plants.

A number of stable transgenic events carrying FRT target sites were produced. These target lines were generated by introducing one of a series of constructs including,

for example, PHP9643, PHP10616, PHP11407, PHP11410, PHP11457, PHP11599, PHP11893 or PHP14220 (See Table 2) into corn cells, either by particle bombardment, as described in Register *et al.* (1994) *Plant Mol. Biol.* 25:951-961 or via *Agrobacterium* co-cultivation as described by Heath *et al.* (1997) *Mol. Plant-Microbe Interact.* 10:22-227;

5 Hiei *et al.* (1994) *Plant J.* 6:271-282 and Ishida *et al.* (1996) *Nat. Biotech.* 14:745-750, and in U.S. Provisional Application Serial No. 60/045,121 to "Agrobacterium Mediated Sorghum Transformation", filed April 30, 1997. All vectors were constructed using standard molecular biology techniques as described for example in Sambrook *et al.*, (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory: Cold

10 Spring Harbor, N.Y.). Table 2 below describes the components within each of the vectors used to create a set of target lines. The assembly strategy was as follows. The first expression unit in each case contains the 2.0 kb PstI fragment of the maize ubiquitin promoter Ubi-1 (Christensen *et al.* (1992) *Plant Mol. Biol.* 18:675-689). Downstream of the ubiquitin promoter, varying FRT sequences were inserted using NcoI or other sites that

15 retained the ATG start codon. PHP10616 has the mo-PAT (U.S. Provisional Patent Application Serial No. 60/035,560 to "Methods for Improving Transformation Efficiency", filed January 14, 1997) coding sequence fused in frame at the XhoI site flanking FRT1 (see above, SEQ ID NO 2). PHP11407 and PHP11893 have GFPm-C3 (PCT/US97/07688 filed May 1, 1997 from Provisional Application 60/016,345 filed May 1, 1996) containing

20 the second intron from potato ST-LS1 (Vancanneyt *et al.* (1990) *Mol. Gen. Genet.* 220:245-250) fused in frame at the XhoI site of FRT1 and FRT6, respectively. The potato proteinase inhibitor II (PinII) terminator (bases 2 to 310 from An *et al.* (1989) *Plant Cell* 1:115-122) was ligated downstream of the coding sequences. PHP10616 has an FRT5 sequence (SEQ ID NO 3) cloned downstream of the PinII terminator.

Table 2

PHP	Upstream-1	Coding-1	Downstream-1	Upstream-2	Coding-2	Downstream-2	Coding-3	Downstream-3
9643	Ubiquitin	ATG/FRT1		E3SS/3SS/O'/ADH intron	moPAT	35S term	NoATG/FRT1/GFP	pinII, FRT5
10616	Ubiquitin	ATG/FRT1/moPAT	pinII, FRT5				m	
11407	Ubiquitin	ATG/FRT1/GFPm-C3-intron	pinII	Ubiquitin	HM1	pinII, FRT5		
11410	Ubiquitin	ATG/FRT5		E3SS/3SS/O'/ADH intron	BAR	35S term, FRT1		
11457	Ubiquitin	ATG/FRT6		E3SS/3SS/O'/ADH intron	BAR	35S term, FRT1		
11599	Ubiquitin	ATG/FRT6		3SS/O'/ADH intron	BAR	35S term, FRT1		
11893	Ubiquitin	ATG/FRT6/GFPm-C3-intron	pinII	Ubiquitin	HM1	pinII, FRT1		
14220	Ubiquitin/FRT1 in 5' UTR	FLPm	pinII	Ubiquitin	GFPm	pinII, FRT5		
	Ubiquitin/FRT1 in intron	FLPm	pinII	Ubiquitin	GFPm	pinII, FRT5		

The second expression units have the maize ubiquitin promoter or alternatively either the enhanced or the standard versions of the cauliflower mosaic virus 35S promoter.

The standard 35S promoter includes bases -421 to +2 (from Gardner *et al.* (1981) Nucl. Acids Res. 9:2871-2888), and the enhanced version has a duplication of bases -421 to -90
5 upstream of this standard 35S promoter. The 79 bp tobacco mosaic virus leader O' (Gallie *et al.* (1987) Nucl. Acids Res. 15:3257-3273) is inserted downstream of the 35S promoter followed by the first intron of the maize alcohol dehydrogenase ADH1-S gene (Dennis *et al.* (1984) Nucl. Acids Res. 12:3983-3990). Coding sequences in these second expression
10 units include either mo-PAT, *bar* (Thompson *et al.* (1987) EMBO J. 6:2519-2523), or *HMI* (Johal and Briggs, Science 258:985-987) genes followed by either the PinII terminator or the 35S terminator (nucleotides 7487-7639 in Gardner *et al.* (1981) Nucl. Acids Res. 9:2871-2888). Varying FRT sites are ligated downstream of the terminators as shown in the table. A third expression unit is present in PHP9643 and has an
15 FRT1/GFPm fusion cloned using the flanking NheI site of FRT1 (SEQ ID NO 2) to remove the ATG start codon of GFPm, thereby making it non-functional in the existing construct, but where correct excision of sequences between FRT1 (SEQ ID NO 2) sites can bring the GFPm in frame with the ubiquitin promoter and ATG of the first expression unit, thereby making it functional. Downstream of GFPm is the PinII terminator followed by
20 an FRT5 sequence (SEQ ID NO 3).

PHP9643 was cloned into a pUC derived plasmid backbone. All other vectors were cloned into a pSB11 (See, for example, EPA0672752A1, EPA0604662A1, EPA0687730A1 and U.S. Patent No. 5,591,616) type plasmid with the expression units contained between the TDNA border sequences. All are oriented with expression unit one
25 adjacent to the right border. The pSB11-based plasmids were integrated into the super binary plasmid pSB1 (See, for example, EPA0672752A1, EPA0604662A1, EPA0687730A1 and U.S. Patent No. 5,591,616) by homologous recombination between the two plasmids. *E. coli* strain HB101 containing the pSB11 derivatives was mated with *Agrobacterium* strain LBA4404 harboring pSB1 to create the cointegrate plasmids
30 PHP10616, PHP11407, PHP11410, PHP11457, PHP11599, PHP11893 and PHP14220 in *Agrobacterium* (by the method of Ditta *et al.* (1980) Proc. Natl. Acad. Sci. USA 77:7347-7351). The cointegrates were verified by *Agrobacterium* resistance to spectinomycin and SalI restriction digests.

Table 2 also includes one example of a vector for creating a target line where the FRT sites are inserted in the maize ubiquitin intron (last entry) as an alternative location for placement of FRT or other target sites.

Following selection of stably transformed events, samples of these target lines were cryopreserved as a supply for future experiments using the approach described by Peterson (see application 08/859,313). For several but not all events, another sample of callus from several of the stable transgenic events was grown, transferred onto regeneration medium to induce plantlet formation and plants were subsequently recovered and grown to maturity (Register *et al.* (1994) *Plant Mol. Biol.* 25:951-961).

10

Example 5. Demonstration of functionality of novel FRT sites in plants.

(A) Excision of DNA sequences between two identical FRT sites, but not when flanked by two non-identical FRT sequences

The extent of intra-plasmid recombination was examined in plants using the FRT excision constructs described in Table 3 below. The vectors PHP10968, PHP10998, PHP10969, PHP11272, PHP11243, PHP11244, PHP12140, PHP12141, PHP12156, and PHP12157 were constructed by ligating the maize Ubiquitin promoter upstream of FRT sequences using NcoI or other sites that maintained the ATG start codon. The FRT sequence was fused in frame at the flanking XhoI site to a GFPm sequence containing a serine to threonine mutation at amino acid residue 65 in the wild type sequence (new sequence termed GFPm-S65T). The pinII terminator was cloned downstream of GFPm.

The second expression unit consists of a promoterless FRT, cloned with the 5' flanking NheI site to remove the ATG start codon, fused in frame to the GUS coding sequence (Jefferson *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83: 8447-8451) and followed by the pinII terminator. The vector backbone is a pUC derived plasmid in all cases. Experiments were conducted by bombarding the indicated plasmids into maize cells along with construct PHP5096, which carries a functional expression cassette for FLP protein. PHP5096, the FLPm expression vector that was used in experiments with the excision and substrate vectors, consists of the maize Ubiquitin promoter cloned upstream of the FLPm coding sequence (U.S. Patent Application Serial No. 08/972,258 to "Novel Nucleic Acid Sequence Encoding FLP Recombinase") and the pinII terminator in a pUC derived plasmid backbone.

In each case, successful excision would remove intervening sequences between the indicated FRT sites thereby bringing an inactive *uidA* (GUS) gene in frame with and in proximity to the ubiquitin promoter resulting in GUS activity. If excision does not occur,

no GUS expression is expected. The results for GUS expression from these experiments are indicated in Table 4 below. In these studies efficient excision occurred only where constructs contained two identical FRT sites. In the case of the FRT6 (SEQ ID NO 4) and FRT7 (SEQ ID NO 5) combination, a small amount of recombination was observed, again

5 emphasizing the need for testing target site combinations and judiciously selecting appropriate combinations for the application.

Table 3

PHP	Upstream-1	Coding-1	Downstream-1	Upstream-2	Coding-2	Downstream-2
10968	Ubiquitin	ATG/FRT1/GFPm-S65T	PinII		noATG/FRT1/GUS	pinII
10998	Ubiquitin	ATG/FRT5/GFPm-S65T	PinII		noATG/FRT5/GUS	pinII
11272	Ubiquitin	ATG/FRT6/GFPm-S65T	PinII		noATG/FRT6/GUS	pinII
12157	Ubiquitin	ATG/FRT7/GFPm-S65T	PinII		noATG/FRT7/GUS	pinII
10969	Ubiquitin	ATG/FRT1/GFPm-S65T	PinII		noATG/FRT5/GUS	pinII
11243	Ubiquitin	ATG/FRT1/GFPm-S65T	PinII		noATG/FRT6/GUS	pinII
12140	Ubiquitin	ATG/FRT1/GFPm-S65T	PinII		noATG/FRT7/GUS	pinII
11244	Ubiquitin	ATG/FRT5/GFPm-S65T	PinII		noATG/FRT6/GUS	pinII
12141	Ubiquitin	ATG/FRT5/GFPm-S65T	PinII		noATG/FRT7/GUS	pinII
12156	Ubiquitin	ATG/FRT6/GFPm-S65T	PinII		noATG/FRT7/GUS	pinII
12933	Ubiquitin/FRT1 in 5' UTR	GFPm-S65T	PinII	FRT1 in 5' UTR/Ubi intron	GUS	pinII
14076	Ubiquitin/FRT1 in intron	AHAS	PinII	FRT1 in Ubi intron	GUS	pinII
14053	Ubiquitin/FRT1 in intron	AHAS	PinII	FRT5 in Ubi intron	GUS	pinII
14086	Ubiquitin/FRT1 in intron	AHAS	PinII	FRT6 in Ubi intron	GUS	pinII

Table 4

Plasmid	Recombination tested between	GUS expression
PHP10968	FRT1 and FRT1	+++
PHP10998	FRT5 and FRT5	++
PHP11272	FRT6 and FRT6	+++
PHP12157	FRT7 and FRT7	+++
PHP9643	FRT1 and FRT5	-
PHP11243	FRT1 and FRT6	-
PHP12140	FRT1 and FRT7	-
PHP11244	FRT5 and FRT6	-
PHP12141	FRT5 and FRT7	-
PHP12156	FRT6 and FRT7	+

5

B) Transient integration of a second DNA sequence flanked by two non-identical FRT sequences into plant cells

Summarized in Table 5 below are data from experiments in which target lines created using the plasmids described in Table 2 were bombarded with a substrate plasmid containing a GUS reporter gene flanked by the corresponding FRT sites used in the target constructs. This experiment measured the ability to detect transient GUS expression shortly after introduction of the substrate plasmid. Since there is no promoter in front of the first coding sequence in the substrate plasmids, random integration, unless occurring in frame behind an appropriate regulatory sequence elsewhere in the genome, would not result in GUS expression. This assay system then evaluates the ability to target FRT-flanked genes into FRT sites in the genome. In general, FRT substrate vectors (Table 6) are constructed as promoterless FRT/gene fusions cloned using the 5' flanking NheI site of the FRT to remove the ATG start codon. Genes fused in frame to the FRT with the flanking XhoI site include one of several scorable or selectable marker genes such as *aadA* (Svab *et al.* (1990) Plant Mol. Biol. 14: 197-205), *uidA*, GFPm, GFPm-C3/intron or *bar* and are followed by a *pinII* terminator. In some cases (PHP10259, PHP10603, PHP11561, and PHP11633), plasmids contain a single expression unit and the second heterologous FRT site is cloned downstream of the *pinII* terminator. Substrate plasmids PHP10859, PHP10997, PHP11204, PHP11699, and PHP12190 have in addition to the first expression unit described above, a second unit consisting of the maize ubiquitin promoter, the

enhanced 35S promoter or a chimeric promoter consisting of the 35S enhancer region cloned upstream of a synthetic core promoter termed Rsyn7 (U.S. Patent Application Serial No. 08/661,601 filed June 11, 1996) cloned upstream of either the HM1, aadA, GUS, or bar coding sequences and the *pinII* terminator. A heterologous FRT is inserted downstream of the second terminator. Finally, PHP11003 and PHP11809 contain three expression units. The first unit is a promoterless noATG/FRT/gene fusion as described above, the second unit contains either the chimeric 35S enhancer/Rsyn7 promoter described above or the ZmdJ1 promoter (Baszczynski *et al.* (1997) *Maydica* 42:189-201) cloned upstream of the GUS coding sequence and the *pinII* terminator. The third expression unit consists of the maize ubiquitin promoter cloned upstream of the HM1 coding sequence, *pinII* terminator and a heterologous FRT sequence. All FRT substrate vectors are cloned into a pUC derived plasmid backbone. Details of the components of these vectors are described in Table 6. Also listed in Table 6 are two vectors with alternative placement of FRT sites in the ubiquitin 5' UTR or intron.

Table 5

# of GUS Spots	PHP9643 (n=74)	PHP11147 (n=127)	PHP11410 (n=32)	PHP11407 (n=38)	PHP11457 (n=113)
no spots	17.57%	3.15%	6.25%	2.63%	7.96%
1-25	22.97%	48.03%	62.50%	10.53%	27.43%
26-100	31.08%	37.80%	18.75%	18.42%	32.74%
101-200	14.86%	8.66%	12.50%	57.89%	27.43%
too many to count	13.51%	2.36%	0.00%	10.53%	4.42%

Table 6

PHP	Coding-1	Downstream-1	Upstream-2	Coding-2	Downstream-2	Upstream-3	Coding-3	Downstream-3
10259	NoATG/FRT1/aadA	pinII, FRT5						
10603	NoATG/FRT1/GUS	pinII, FRT5						
10839	NoATG/FRT1/GFPm	PinII	Ubiquitin	HM1	pinII, FRT5			
10997	NoATG/FRT5/GUS	PinII	Ubiquitin	aadA	pinII, FRT5			
11003	NoATG/FRT1/GFPm	PinII	E3SS/Rsyn7/O'/ADH intron	GUS	pinII	Ubiquitin	HM1	pinII, FRT5
11204	NoATG/FRT1/BAR	PinII	E3SS/Rsyn7/O'/ADH intron	GUS	pinII, FRT5			
11561	NoATG/FRT6/GUS	pinII, FRT1						
11633	NoATG/FRT5/GUS	pinII, FRT1						
11699	NoATG/FRT6/GFPm-C3-intron	PinII	Ubiquitin	HM1	pinII, FRT1			
11809	NoATG/FRT6/GFPm-C3-intron	PinII	P3.7	GUS	pinII	Ubiquitin	HM1	pinII, FRT1
12190	NoATG/FRT1/GUS	PinII	E3SS/3SS/O'/ADH intron	BAR	pinII, FRT5			
			Ubiquitin/FRT1 in 5' UTR	HM1	pinII	E3SS/3SS/O'/ADH intron	BAR	pinII, FRT5
			Ubiquitin/FRT1 in intron	HM1	pinII	E3SS/3SS/O'/ADH intron	BAR	pinII, FRT5

Results in Table 5 indicate that the frequency and level of GUS expression varies among different events, as might be predicted for genes inserted in different positions in the genome. The prediction is that once a high frequency, high expressing line is identified, that the expression of genes subsequently introduced into those same sites will also be higher than in other lower expressing events.

C) Stable integration of a second DNA sequence flanked by two non-identical FRT sequences into plant cells

A subset of the stable transgenic "target lines" described in example 4 above was used in experiments aimed at stably retargeting into these primary target lines a new gene flanked by the same FRT sites used in the target lines and cloned in a second construct 'substrate' plasmid. Table 7 lists the constructs contained in the primary target lines (from Table 2), the FRT sites contained in these lines and the substrate plasmids (from Table 6) that were subsequently retargeted into the target lines.

Table 8 presents data from stable transgenic events which demonstrate successful and reproducible targeting of introduced sequences to previously created genomic target sites. The data shown are for 18 independent target lines, each retargeted with a promoterless GUS construct. Since the bar gene was concurrently introduced on the same plasmid, the proportion of GUS expressing events from the total events recovered on bialaphos selection provides a measure of retargeting frequency relative to random integration.

Table 7

Target construct	FRT Sites	Substrates being evaluated
PHP9643	1/1/5	10603, 10259, 10859, 10997, 11003
PHP11147	1/5	10603, 10859, 11003
PHP11407	1/5	10603, 11204, 12190
PHP11410	5/1	11633
PHP11457	6/1	11561, 11699, 11809
PHP11893	6/1	Experiments in progress

Table 8

Target Line	# of Random Events	# of Targeted Events	Targeting Frequency (%)
A	13	1	7.1
B	14	1	6.7
C	108	14	11.5
D	18	1	5.3
E	14	2	12.5
F	9	1	10.0
G	65	1	1.5
H	63	9	12.5
I	71	6	7.8
J	15	1	6.3
K	33	9	21.4
L	19	2	9.5
M	8	1	11.1
N	12	1	7.7
O	29	4	12.1
P	43	4	8.5
Q	16	3	15.8
R	4	1	20.0
S	12	1	7.7
T	10	1	9.1
U	1	2	66.7

Example 6. Evaluation of impact of introduced FRT sequences on plant development, gene expression and agronomic performance.

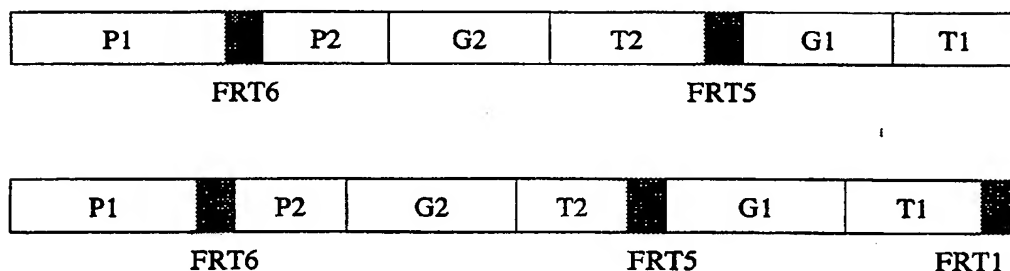
Initial evaluation of the impact of the introduced sequences on plant growth and gene expression is conducted in the greenhouse by making regular observations through to pollination and seed set. Plants are both selfed and crossed to other genotypes to obtain T1 seed for subsequent greenhouse and field evaluation. For gene expression evaluation, both qualitative and quantitative data are collected and analyzed. T1 seeds from transgenic events which give acceptable or desirable levels of expression and which show no significant negative impact on plant development (e.g., have normal developmental morphology, are male and female fertile, etc.) are then grown in managed field plots along with non-transgenic control plants, and standard agronomic performance data is collected and evaluated.

Example 7. Conversion of an introduced functional FRT sequence into a second non-identical functional FRT sequence

The approach taken here to develop a method for converting between different FRT sites for use in various applications is based on the previously described 'chimeraplasty' strategy for making specific targeted nucleotide modifications at a specified extrachromosomal or genomic target sequence in animal cells (Yoon *et al.* (1996) *Proc. Natl. Acad. Sci.* 93:2071-2076; Cole-Strauss *et al.* (1996) *Science* 273:1386-1389). This capability in plants, as demonstrated recently in our laboratories and described in U.S. Patent Application Serial No. 60/065,628, filed November 18, 1997, is beneficial to extending the potential use of the present invention for broader application. The proposed use of this 'chimeraplasty' technology in the present invention would be to target and modify nucleotides in one FRT site of a pair of non-identical FRT sites flanking a DNA sequence of interest in a way that then makes the two FRT sites identical. Subsequent or concurrent expression of FLP recombinase in cells with these FRT site modifications would lead to excision of the sequences between these now identical FRT sites, thereby removing specifically the undesirable DNA sequences from the previously created stable transgenic event containing those sequences. An application of this approach would be for example in the case of a selectable marker which is required during initial steps of a breeding or backcrossing program to maintain and select for preferred individual plants, but which is not desired in the final product.

A) Vector design and construction for testing chimera-plasty-based FRT site conversion

The target vectors for evaluating this FRT site modification strategy are shown generically below, where P1 and P2 represent two different promoters, G1 and G2 represent two genes, and T1 and T2 represent two terminator regions; these regions are shown as white boxes. Different FRT sites are indicated and shown as dark boxes. One version of the construct incorporates a third unique FRT site downstream of the second gene and is used to evaluate whether the targeted conversion, in this case, of FRT5 to FRT6 (SEQ ID NO 4), also results in conversion of the downstream FRT1 (SEQ ID NO 2) site to an FRT6 (SEQ ID NO 4) site. In the former case, expression of the downstream gene (G1) should be detected, while if the conversion is not specific to FRT5 (SEQ ID NO 3) and the FRT1 (SEQ ID NO 2) site is converted also, then both gene activities will be lost. For the specific examples used here P1 is the maize ubiquitin promoter, P2 is the enhanced CaMV 35S promoter, G1 is the *uidA* (GUS) gene, G2 is the *bar* gene, and T1 and T2 are *pinII* terminators. It is understood that based on the various descriptions of vector constructs earlier in this application, a variety of different promoters, genes, terminators or DNA sequences or FRT sites could be used in practicing this component method. The DNA cassettes as shown below could be assembled into either a pUC-based plasmid for direct DNA delivery methods (such as particle bombardment) or into a binary vector for *Agrobacterium*-based transformation as described previously.



B) Design of chimeric oligonucleotide molecules for chimera-plasty-based targeted conversion of an FRT site

Shown below are specific examples of chimeric molecules that would be used to modify a single nucleotide so as to convert the FRT5 (SEQ ID NO 3) site to an FRT6 (SEQ ID NO 4) site in constructs as described above. Both the linear sequence of these

chimeric molecules as well as the predicted active form of the molecule (based on the Yoon *et al.* and Cole-Strauss *et al.* publications above) are shown. DNA residues are represented in upper case, RNA residues in lower case, and the site to be modified (a single nucleotide difference between FRT5, SEQ ID NO 3, and FRT6, SEQ ID NO 4) is underlined and in bold. Two examples of chimeras are presented below differing in the number of residues downstream of the FRT5 (SEQ ID NO 4) site that would be included in the chimeric molecule design and which would thus determine the specificity to the target sequence.

- 10 1. **Chimeric oligonucleotide linear sequence** (sequence includes six target-specific residues downstream of the FRT site being modified in the target construct and should convert only this single specific FRT5, SEQ ID NO 3, site to an FRT6, SEQ ID NO 4, site)

15 5' - CCTATTCTTCAAAAAGTATAGGA¹CTTCAGTACTTTTTTaguacugaagu
CCTATACTTTuugaaqaauaqqGCGCGTTTTCGCGC-3'

20 **Active oligonucleotide conformation**

TGCGCG--ggauaagaaguuTTTCATATCCuugaagucaugaT
 T
 T
 25 TCGCGC CCTATTCTTCAAAAAGTATAGGAACTTCAGTACTT
 3' 5'

2. **Chimeric oligonucleotide linear sequence** (sequence contains residues
30 specific to only sequences in the FRT site and so should convert any FRT5,
SEQ ID NO3, site in a target molecule to an FRT6, SEQ ID NO 4, site)

5' -
TATTCTTCAAAAAGTATAGGAAGTCTTTTgaaguuccuaTACTTTuuga
35 agaauaGCGCGTTTTCGCGC-3'

Active oligonucleotide conformation

40 TCGCGC--auaagaaguTTTCATauccuugaagT
T T
T T
TCGCGC TATTCTTCAAAAGTATAGGAACTTCT
3' 5'

45

Vector constructions and chimeric oligonucleotide molecules as described above were generated and used in experiments.

C) Demonstration of conversion from one FRT site to another

5 Stable transgenic maize lines are generated with the constructs as described above or with other related ones by transforming in the constructs and selecting on bialophos as described before. Tissues to be used for chimera delivery are transferred onto non-bialophos-containing media and the chimeric oligonucleotides are delivered into cells of these stable events by particle bombardment, together with co-delivery of PHP5096 which
10 carries a functional FLP recombinase expression cassette. In control experiments, only chimeric molecules or only PHP5096 are delivered. After sufficient time for cells to recover without bialophos selection, samples of the bombarded events are evaluated for GUS expression. For those bombarded events containing the construct with the downstream FRT1 (SEQ ID NO 2) site which do not show GUS expression, an equivalent
15 sample of cells are plated and grown on medium with or without bialophos selection to assess sensitivity to the chemical. If the chimeric molecules are specific for modifying only the FRT5 (SEQ ID NO 3) site, then no differences in number and growth of cells should be observed between treatments with or without selection. Otherwise, reduced growth and recovery should be noted.

20

D) Molecular verification of stable conversion of FRT sites

DNA from those samples that exhibit GUS expression is isolated, amplified by PCR if necessary, and sequenced by standard methods through the region corresponding to the predicted nucleotide conversion. A sufficient stretch of DNA is sequenced to cover
25 the entire originally introduced region of DNA so as to confirm correct and specific conversion. Using standard methods for PCR, Southern analysis and/or sequencing of GUS expressing and non-expressing samples establishes the presence or absence of specific DNA fragments prior to and following chimeric molecule and FLP recombinase delivery, and thus substantiates the visual and biochemical observations made above.

30

E) Utility of chimeraplasty-based FRT site conversion in a transgene stacking strategy for plants

Described in Figure 1 is one potential strategy for combining or stacking multiple desired transgenes at one genomic location using the non-identical FRT-based system of

the present invention. While stacking of genes can be achieved without the use of the targeted FRT conversion method described in this example 7, this latter method extends the capabilities of the system by allowing *in vivo* conversion of FRT sites to create new sites, rather than re-introducing new FRT sites by transformation. In the diagram of Figure 1, an FRT site with an asterisk beside it indicates that it was initially created to be non-functional with respect to recombination between it and the equivalent FRT site without an asterisk, but which upon conversion with the chimeraplasty-based approach described herein renders it capable of recombination with its equivalent non-asterisk counterpart. In the specific example presented in the figure, this would facilitate for example removal of a selectable marker either to no longer have it present, or to allow one to re-use the selectable marker in future transformations. Thus this method also provides a mechanism to recycle selectable markers, as is possible in using the FRT system of the present invention alone.

15

Discussion

To date in plants, the major application of the FLP/FRT system has been for DNA excision (Lyznik *et al.* (1993) *Nucleic Acids Res.* 21:969-975). For example, a gene such as a selectable marker flanked by FRT sites is first introduced into plant cells by one of several transformation approaches, and stable transgenic events or plants are recovered via appropriate selection. Then in order to eliminate the selectable marker gene, FLP protein is expressed in the cells either transiently by introducing a plasmid carrying a FLP expression cassette, stably following integration of an introduced FLP expression cassette, or by crossing plants carrying the FRT-flanked selectable marker gene with plants carrying sequences for and expressing active FLP protein (U.S. Patent Application Serial No. 08/972,258 to "Novel Nucleic Acid Sequence Encoding FLP Recombinase").

A major problem associated with developing the FLP/FRT system for integrating genes into animals or plants stems from the fact that the recombination reaction catalyzed by yeast FLP recombinase is a reversible process (Sadowski (1995) in Progress in Nucleic Acid Research and Molecular Biology 51:53-91). For example, following introduction of a DNA sequence flanked by similarly oriented FRT sites into plant cells in the presence of actively expressing FLP recombinase, recombination should lead to insertion of the new DNA sequences at the endogenous FRT site. However, with continued expression of FLP enzyme, the reverse reaction would lead to re-excision of the introduced sequences because of recombination between the identical FRT sites. Since the reaction is reversible,

integration and excision can repeatedly continue towards equilibrium. As cells divide and the DNA substrate concentration per cell decreases, the probability of integration decreases, such that in general, as long as active FLP protein is expressed the reaction will be driven towards the non-integrated state. To favor integration, a situation must be established which precludes re-excision once integration occurs. A number of strategies have been suggested, including limiting the duration of activity of FLP recombinase through inducible expression or by directly introducing FLP protein or RNA into cells (Sadowski (1995) Progress on Nucleic Acid Research and Molecular Biology 51:53-91), but to date no routine non-random integration system has been established for plants.

The present invention describes the development of a useful new gene targeting system for plants which utilizes the yeast FLP recombinase or a modified FLP recombinase designed to work more efficiently in certain plant species and novel non-identical FRT sites which can be used for directional non-reversible DNA integration. Additionally, described herein is a novel use of accessory technologies such as 'chimeraplasty' permitting *in vivo* or *in vitro* modification of DNA sequences, such as FRT sites to further extend the utility of the system. Data provided demonstrate the successful stable integration of DNA sequences between two previously introduced non-identical FRT sites in maize. We show also that the DNA sequences between the FRT sites can be subsequently replaced by a second DNA sequence flanked by the same FRT sites as the first. Together these results demonstrate that it is possible to introduce and recover pairs of non-identical FRT sites at certain genomic locations, that one can select desirable or preferred genomic locations for expressing DNA sequences of interest, and that these selected locations can be used to re-target other DNA sequences of interest. Apart from the obvious benefits of being able to integrate genes into the genome of plants, the present invention provides a means for facilitating the introduction of novel genes or DNA sequences into genomic locations previously determined to be particularly beneficial for gene integration from the perspective of providing suitable levels of stable expression of the introduced gene(s) and not exhibiting deleterious impacts on agronomic characteristics including yield. In addition the invention provides a system whereby integration of two or more genes can be targeted to the same genomic location, providing a mechanism for 'gene stacking'. These stacked genes can then be maintained and managed as a closely linked pair of traits in breeding programs. Thus this invention also provides an improved method for introducing, maintaining and breeding multiple genetic traits of interest, including agronomic traits, commercially important genes or other heterologous gene products.

The invention further proposes to use the non-recombination feature of non-identical FRT sites to allow creation of a set of 'parental' lines, which are initially well-characterized for all the desired expression and performance parameters described above.

5 These lines then serve as the basis for introduction of new traits into the same predefined sites in the genome where the initial genes were introduced. Many fewer events would need to be generated, since integration would preferentially occur in sites shown to express well and have minimal negative impact on performance.

10 All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

15 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

THAT WHICH IS CLAIMED:

- 5 1. A method for targeting the insertion of nucleotide sequences of interest to a specific chromosomal site within a plant genome, said method comprising:
- a) transforming said plant with a transfer cassette, said transfer cassette comprising said nucleotide sequence of interest flanked by non-identical recombination sites;
- 10 b) wherein said plant genome comprises a target site flanked by non-identical recombination sites which correspond to the flanking sites of said transfer cassette; and,
- c) providing a recombinase that recognizes and implements recombination at the non-identical recombination sites.
- 15 2. The method of Claim 1, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX sites.
- 20 3. The method of Claim 2, wherein said sites are a FRT site and a mutated FRT site.
4. The method of Claim 1 wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide
- 25 sequence encoding said recombinase.
5. The method of Claim 3, wherein said recombinase is FLP.
6. The method of Claim 5, wherein said FLP has been synthesized using
- 30 maize preferred codons.
7. The method of Claim 3, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

8. A transformed plant comprising within its genome a target site comprising at least two non-identical recombination sites.

5 9. The transformed plant of Claim 8, wherein said non-identical recombination sites are FRT sites.

10 10. The transformed plant of Claim 8, wherein said sites are a FRT site and a mutated FRT site.

11. The transformed plant of Claim 10, wherein said plant is a dicot.

12. The transformed plant of Claim 10, wherein said plant is a monocot.

13. The transformed plant of Claim 12, wherein said monocot is maize.
15

14. The transformed plant of Claim 10, wherein said mutated FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

15. Seed of the plant of Claim 8.
20

16. Seed of the plant of Claim 12.

17. Seed of the plant of Claim 13.

25 18. A method for locating preferred integration sites within a plant genome, said method comprising transforming a plant with a target nucleotide flanked by non-identical recombination sites and determining the level of expression of said target nucleotide, determining the impact of the genomic position of the target nucleotide on the agronomic performance of the plant, and selecting the preferred integration sites.

30

19. The method of Claim 18, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX sites.

20. The method of Claim 19, wherein said sites are a FRT site and a mutated FRT site.

21. The method of Claim 18, wherein said recombinase is provided by
5 genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

22. The method of Claim 20, wherein said recombinase is FLP.

10 23. The method of Claim 22, wherein said FLP has been synthesized using maize preferred codons.

24. The method of Claim 20, wherein said mutant FRT site is FRT 5 (SEQ
ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).
15

25. A method for assessing promoter activity in a plant cell, said method comprising:

a) transforming said plant with a transfer cassette, said cassette comprising
a promoter operably linked to a nucleotide sequence encoding a marker gene and
20 flanked by non-identical recombination sites;

b) wherein said plant genome comprises a target site flanked by non-
identical recombination sites which correspond to the flanking sites of said transfer
cassette; and,

c) providing a recombinase that recognizes and implements recombination
25 at the non-identical recombination sites.

26. The method of Claim 25, wherein said non-identical recombination sites
are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX
sites.
30

27. The method of Claim 26, wherein said sites are a FRT site and a
mutated FRT site.

28. The method of Claim 25, wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

5 29. The method of Claim 27, wherein said recombinase is FLP.

30. The method of Claim 29, wherein said FLP has been synthesized using maize preferred codons.

10 31. The method of Claim 27, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

32. A method to minimize or eliminate expression resulting from random integration of DNA sequences by:

15 a) creating a genomic target site comprising one or more identical or non-identical recombination sites positioned downstream of a promoter fused to an ATG translation start sequence,

b) introducing a substrate vector comprising gene sequences wherein the ATG translation start sequence of the gene has been replaced with a corresponding recombination site positioned downstream of the ATG translation start sequence of the genomic target site, and in a manner such that following successful targeting, the gene sequences are positioned in the correct reading frame of a translational fusion between the ATG of the genomic target site, the recombination site and the gene sequences,

20 c) providing a recombinase that recognizes and implements recombination at the recombination sites.

33. The method of Claim 32, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX sites.

30

34. The method of Claim 33, wherein said sites are a FRT site and a mutated FRT site.

35. The method of Claim 32, wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

5 36. The method of Claim 34, wherein said recombinase is FLP.

37. The method of Claim 36, wherein said FLP has been synthesized using maize preferred codons.

10 38. The method of Claim 34, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

39. A method to directly select transformed plant cells, said method consisting of:

15 a) transforming said plant with a transfer cassette, said transfer cassette comprising a nucleotide sequence encoding a selectable marker gene not operably linked to a promoter, flanked by non-identical recombination sites;

b) wherein said plant genome comprises a target site comprising a promoter operably linked to a nucleotide sequence encoding a first non-identical recombination site and a gene coding region and a second non-identical recombination site, wherein
20 said first and second non-identical recombination sites correspond to the flanking sites of said transfer cassette,

c) providing a recombinase that recognizes and implements recombination at the non-identical recombination sites, and growing said plant cells on the appropriate
25 selective agent to recover cells which have successfully undergone targeted integration of the transfer cassette at the target site leading to activation of expression of the selectable marker.

40. The method of claim 39, wherein said transfer cassette comprises at least
30 one additional coding region operably linked to a promoter that drives expression in a plant cell.

41. The method of claim 40, wherein said additional coding region encodes a recombinase that facilitates recombination between the identical sites of the transfer cassette and the plant genome.

5 42. The method of claim 39, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX sites.

10 43. The method of Claim 42, wherein said sites are a FRT site and a mutated FRT site.

44. The method of Claim 41, wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

15

45. The method of Claim 43, wherein said recombinase is FLP.

46. The method of Claim 45, wherein said FLP has been synthesized using maize preferred codons.

20

47. The method of Claim 43, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

25 48. The method of claim 39, wherein said plant cell is a monocot plant cell.

25

49. The method of claim 48, wherein said monocot is maize.

50. The method of claim 39, wherein said plant cell is a dicot plant cell.

30

51. The method of claim 50, wherein said dicot is canola, Brassica, soybean, sunflower, and cotton.

52. A DNA construct comprising an intron, a gene coding region, a terminator region and one or more non-identical recombination sites, wherein one non-identical recombination site is contained within said intron.

5 53. The DNA construct of claim 52 comprising a promoter operably linked to the gene coding region.

54. The nucleotide sequence of claim 53, wherein said intron is selected from the group consisting of an ubiquitin intron, an Adh intron, and a DnaJ intron.

10

55. The nucleotide sequence of claim 54, wherein the ubiquitin intron is the first intron from a maize ubiquitin gene.

56. The nucleotide sequence of claim 54, wherein the Adh intron is the first
15 intron from a maize Adh gene.

57. The nucleotide sequence of claim 54, wherein the DnaJ intron is the first intron from a maize DnaJ gene.

20 58. A method for reducing the complexity of integration of transgenes in an organism, said method comprising:

a) transforming an organism with a transfer cassette flanked by non-identical recombination sites and,

b) providing a recombinase that recognizes and implements recombination
25 at the non-identical recombination sites and,

c) analyzing and selecting those organisms with simple integration patterns in their genome.

59. The method of claim 58, wherein the recombinase is integrated in the
30 genome of said organism.

60. The method of claim 58, wherein the transfer cassette further comprises at least one additional coding region operably linked with a promoter that drives expression in a plant.

35

61. The method of claim 60, wherein said additional coding region encodes a recombinase that facilitates recombination between the identical sites of the transfer cassette and the plant genome.

5 62. The method of claim 58, wherein the recombinase is provided on second transfer cassette.

63. The method of Claim 61, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX
10 sites.

64. The method of Claim 62, wherein said sites are a FRT site and a mutated FRT site.

15 65. The method of Claim 61, wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

20 66. The method of Claim 63, wherein said recombinase is FLP.

67. The method of Claim 66, wherein said FLP has been synthesized using maize preferred codons.

25 68. The method of Claim 63, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

69. The method of claim 58, wherein said organism is a eukaryote.

30 70. The method of claim 69, wherein said eukaryote is a plant.

71. The method of claim 70, wherein said plant is a monocot.

72. The method of claim 71, wherein said monocot is maize.

73. The method of claim 70, wherein said plant is a dicot.

74. The method of claim 73, wherein said dicot is canola, Brassica, soybean, sunflower, and cotton.

5

75. A method to combine multiple transfer cassettes at one location in a genome of an organism, said method comprising:

- a) transforming an organism with a first transfer cassette comprising at least three non-identical recombination sites, wherein at least two of said non-identical recombination sites, herein referred to as the first retargeting sites, are in near proximity to each other; and
- b) transforming said organism with a second transfer cassette flanked by two non-identical recombination sites which correspond to the first retargeting sites of said first transfer cassette, and
- 15 c) providing a recombinase that recognizes and implements recombination at the first retargeting sites; and
- d) repeating steps b) and c) to combine the desired number of transfer cassettes at one location in the organism's genome.

20 76. The method of claim 75, wherein said first retargeting sites flank a nucleotide sequence encoding a sequence not required in the genome of the organism.

77. The method of claim 76, wherein the nucleotide sequence flanked by the retargeting sites comprise at least one unique non-identical recombination site.

25

78. The method of claim 75, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX sites.

30 79. The method of Claim 78, wherein said sites are a FRT site and a mutated FRT site.

80. The method of Claim 77, wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

5 81. The method of Claim 79, wherein said recombinase is FLP.

82. The method of Claim 81, wherein said FLP has been synthesized using maize preferred codons.

10 83. The method of Claim 79, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

15 84. The method of claim 75, wherein said organism is a plant.

85. The method of claim 84, wherein said plant is a monocot.

86. The method of claim 85, wherein said monocot is maize.

20 87. The method of claim 84, wherein said plant is a dicot.

88. The method of claim 87, wherein said dicot is canola, Brassica, soybean, sunflower, and cotton.

25 89. A method to remove a nucleotide sequence introduced into the genome of an organism as part of a transfer cassette, said method comprising:

- a) transforming said organism with a transfer cassette comprising a nucleotide sequence flanked by non-identical recombination sites;
 - b) introducing into said organism a chimeric RNA-DNA oligonucleotide molecule capable of recognizing and implementing a nucleotide conversion in one of the non-identical recombination sites of the introduced transfer cassette so as to create two identical recombination sites; and
 - c) providing a recombinase that recognizes and implements excision of the sequences between the said two identical recombination sites.
- 30

90. the method of claim 89, wherein said nucleotide sequence comprises a promoter operably linked to a coding sequence for a selectable marker gene.

5 91. The method of claim 89, wherein said non-identical recombination sites are selected from the group consisting of FRT, mutant FRT, LOX, and mutant LOX sites.

10 92. The method of Claim 91, wherein said sites are a FRT site and a mutated FRT site.

93. The method of Claim 90, wherein said recombinase is provided by genetically transforming said plant with an expression cassette containing a nucleotide sequence encoding said recombinase.

15

94. The method of Claim 92, wherein said recombinase is FLP.

95. The method of Claim 94, wherein said FLP has been synthesized using maize preferred codons.

20

96. The method of Claim 92, wherein said mutant FRT site is FRT 5 (SEQ ID NO 3), FRT 6 (SEQ ID NO 4), or FRT 7 (SEQ ID NO 5).

25

97. The method of claim 89, wherein said organism is a plant.

98. The method of claim 97, wherein said plant is a monocot.

99. The method of claim 98, wherein said monocot is maize.

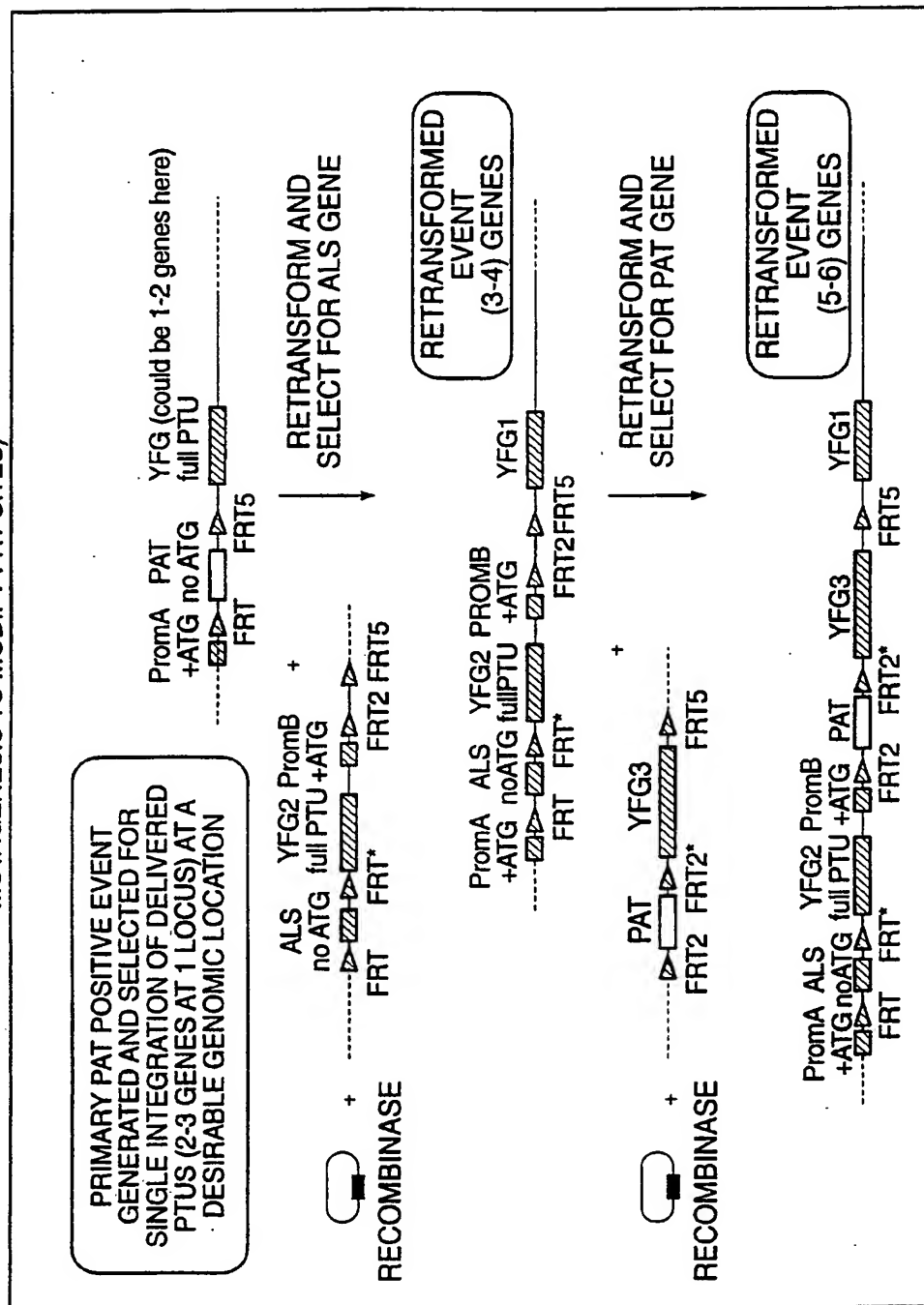
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100. The method of claim 97, wherein said plant is a dicot.

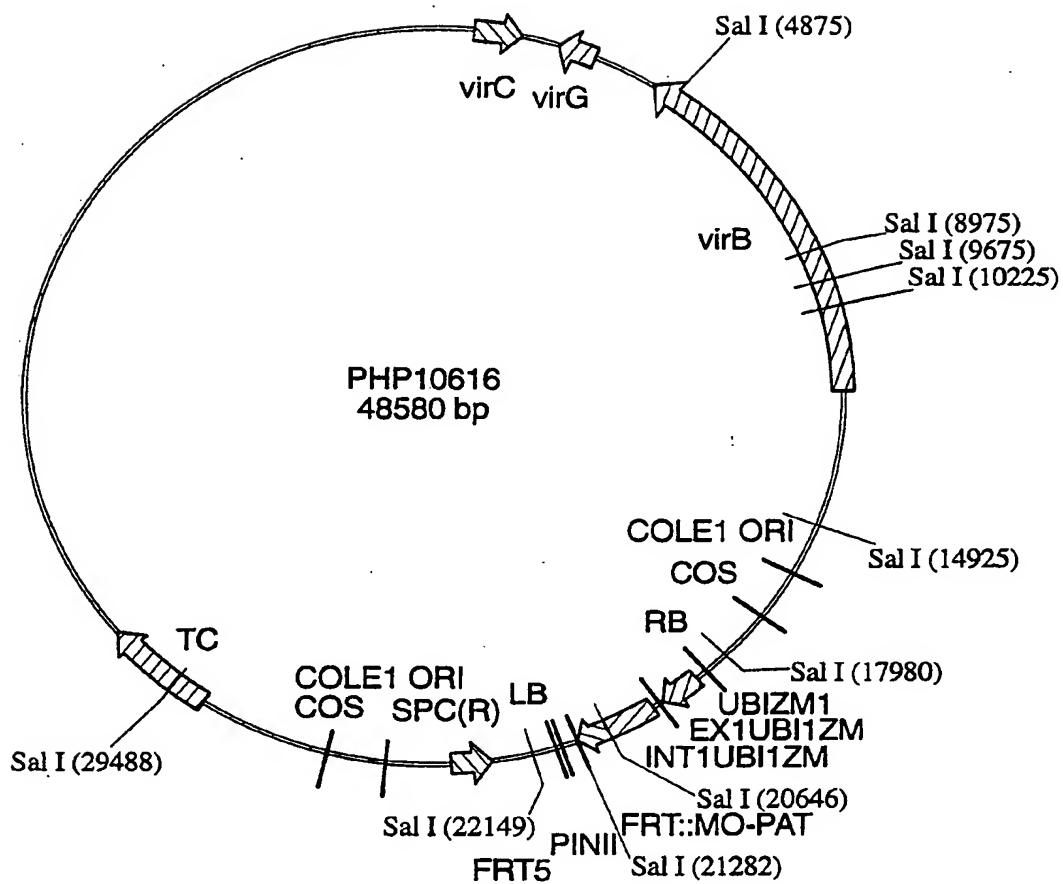
101. The method of claim 100, wherein said dicot is canola, Brassica, soybean, sunflower, and cotton.

ONE SCHEME FOR GENE STACKING VIA SITE-SPECIFIC
INTEGRATION USING THE FLP SYSTEM
(UTILIZES 3 NON-HOMOLOGOUS FRT SITES,
2 SELECTABLE MARKERS, AND OPTIONAL TARGETED
MUTAGENESIS TO MODIFY FRT SITES)

FIG. 1.



2/2



UBI::ATG/FRT1/moPAT/pinII + FRT5

FIG. 2.

SEQUENCE LISTING

<110> Baszczynski, Christopher

Bowen, Benjamin A.

Peterson, David J.

Tagliani, Laura A.

<120> Compositions and Methods for Genetic Modification of
Plants

<130> 035718-158667

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<150> 60/065,627

<151> 1997-11-18

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/24610

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/11 C12N15/63 C12N15/90

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 97 47758 A (MASSACHUSETTS INSTITUTE OF TECHNOLOGY AND AL.) 18 December 1997 *see the whole patent*	1-101
X	--- J. SEIBLER ET AL.: "Double reciprocal crossover by FLP-recombinase: a concept and an assay" BIOCHEMISTRY, vol. 36, 1997, pages 1740-1747, XP002074110 *see the whole document* --- -/-	1-101

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

22 March 1999

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INTERNATIONAL SEARCH REPORT

In ternational Application No

PCT/US 98/24610

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	B. SAUER: "Identification of cryptic lox sites in the yeast genome by selection for Cre-mediated chromosome translocations that confer multiple drug resistance" JOURNAL OF MOLECULAR BIOLOGY, vol. 223, 1992, pages 911-928, XP002097373 *see the whole article* ----	1-101
X	J.F. SENECOFF ET AL.: "DNA recognition by the FLP recombinase of the yeast 2 micron plasmid" JOURNAL OF MOLECULAR BIOLOGY, vol. 201, 1988, pages 405-421, XP002097374 *see the whole article* ----	1-101
X	WO 97 09439 A (GENVEC, INC.) 13 March 1997 *see the whole patent* ----	1-101
X	WO 97 09436 A (CRC FOR PHARMACEUTICAL RESEARCH PTY, LTD.) 13 March 1997 *see the whole patent* -----	1-101

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/24610

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